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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/989,890	11/21/2001	Susana Salceda	DEX-0287	1461
32800	7590	06/01/2006	EXAMINER	
LICATA & TYRRELL P.C. 66 E. MAIN STREET MARLTON, NJ 08053			MARTINELL, JAMES	
			ART UNIT	PAPER NUMBER
			1634	
DATE MAILED: 06/01/2006				

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/989,890

Applicant(s)

SALCEDA ET AL.

Examiner

James Martinell

Art Unit

1634

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 27 September 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-17 is/are pending in the application.
- 4a) Of the above claim(s) 10-13 and 16 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-9, 14, 15 and 17 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date <u>4/03, 2/04 & 10/04</u> . | 6) <input type="checkbox"/> Other: _____ |

Art Unit: 1634

The Art Unit location of your application in the USPTO has changed. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to Art Unit 1634.

The requirement for restriction mailed July 26, 2004 is vacated and is replaced by the requirement for restriction outlined below.

Restriction to one of the following inventions is required under 35 U.S.C. 121:

- I. Claims 1-9, 14/1, 15/1, and 17, drawn to nucleic acids, nucleic acid molecular hybridization assays, vectors, host cells, methods of producing polypeptides, and nucleic acid vaccines, classified in class 536, subclass 23.1, class 435, subclasses 6, 320.1, 325, and 69.1, and class 514, subclass 44.
- II. Claims 10, 11, 14/11, and 15/11, drawn to polypeptides, and polypeptide vaccines, classified in class 530, subclass 350 and class 514, subclass 12.
- III. Claims 12, 13, and 16, drawn to antibodies, antibody assays, and methods of treatment using antibodies, classified in class 530, subclass 387.1, class 435, subclass 7.1, and class 424, subclass 130.1.

The inventions are independent or distinct, each from the other for the following reasons. The nucleic acids, vectors, host cells, and nucleic acid vaccines of Group I are materially different from, and are therefore independent and distinct from the polypeptides and polypeptide vaccines of Group II and the antibodies of Group III. The methods of Group I may be practiced independently of the methods of Group III. The nucleic acids, vectors, host cells, and nucleic acid vaccines of Group I are not needed to practice the methods of Group III. The polypeptides and polypeptide vaccines of Group II are materially different from, and are therefore independent and distinct from the antibodies of Group III. The polypeptides and polypeptide vaccines of Group II are not needed to practice the methods of Group III.

Claims 1-9, 14/1, 15/1, and 17 are drawn to nucleotides, nucleotide constructs, and/or methods requiring the use of nucleotides or nucleotide constructs that contain more than one individual, independent, and distinct nucleotide sequence in alternative form. Accordingly, these claims are subject

Art Unit: 1634

to restriction under 35 U.S.C. § 121 as outlined in 1192 O.G. 68 (November 19, 1996). This notice permits the examination of from one to ten independent and distinct nucleotide sequences in a single application based upon USPTO resources.

Applicant is required to select no more than ONE of the individual sequences for examination. The search of the no more than ONE selected sequence may include the complement of the selected sequence and, where appropriate, may include subsequences within the selected sequence (*e.g.*, oligomeric probes and/or primers).

Claims 10-13, 14/11, 15/11, and 16 are drawn to more than one unrelated, independent, and distinct polypeptide or methods requiring the use of more than one unrelated, independent, and distinct polypeptide. Should applicants elect either one of Groups II or III for examination, applicants are further required to select one polypeptide or a set of methods that requires the use of only one polypeptide for examination on the merits.

Applicants have elected original Group I (claims 1-5, 7, and 8) and SEQ ID NO: 105 encoding SEQ ID NO: 238 for examination in the response filed September 27, 2004. Applicants should note that the requirement for restriction is among independent and distinct inventions and that there is no species election. In order to expedite prosecution of the application, applicants' election of Group I will result in the examination of claims 1-9, 14/1, 15/1, and 17 as they pertain to SEQ ID NO: 105 and nucleic acids that encode SEQ ID NO: 238 or portions thereof in this Office action. Applicants may traverse the requirement for restriction in this Office action in their next response.

Claims 10-13, 14/11, 15/11, and 16 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on September 27, 2004.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Art Unit: 1634

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-9, 14, 15, and 17 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. the claims are vague, indefinite, and incomplete.

- (a) Claim 1 is vague and indefinite because it claims more than was elected.
- (b) The recitation of "comprising a nucleic acid sequence" (claim 1(a) and 1(b)) is vague and indefinite because it is not clear whether applicant intends the phrase to include the entire nucleic acid sequence of SEQ ID NO: 105 or to include all nucleic acids that may include "a" sequence as short as two contiguous nucleotides of SEQ ID NO: 105.
- (c) The recitation of "encodes an amino acid sequence" (claims 1(a)) is vague and indefinite because it is not clear whether applicant intends the phrase to include nucleic acids that encode the entire amino acid sequence of SEQ ID NO: 238 or to include all nucleic acids that may encode an amino acid sequence that includes "a" sequence as short as two contiguous amino acids of SEQ ID NO: 238.
- (d) The recitation of "selectively hybridizes" (claim 1) is vague and indefinite because selective hybridization depends upon the presence of competing binding partners in the reaction mixture. There is no mention of the presence or absence of such competing binding partners in the claims.
- (e) The recitation of "will selectively hybridize" (claim 6) is vague and indefinite because selective hybridization depends upon the presence of competing binding partners in the reaction mixture. There is no mention of the presence or absence of such competing binding partners in the claims.

Art Unit: 1634

- (f) The recitation of "means for determining the presence of the nucleic acid molecule of claim 1" (claim 15) is vague and indefinite because the nature of such "means" is not disclosed or mentioned. The function of "determining the presence of the nucleic acid of claim 1" is so broad as to make the metes and bounds of the "means" for performing the function unclear.
- (g) Claims 14, 15, and 17 are vague, indefinite, and incomplete because they depend from non-elected claim 11.

Claims 1-9, 14, 15, and 17 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The claimed invention is not described adequately in that the claims are broad enough to include any and all nucleic acids that comprise either as few as two contiguous nucleotides of SEQ ID NO: 105 or encode as few as two amino acids of SEQ ID NO: 238 (see items (b) and (c) in the rejection above).

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-3, 7, and 8 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Puttikhunt et al (Molec. Gen. Genet. 247: 118 (1995)). Puttikhunt et al discloses a DNA that encodes amino acids 51-60 of SEQ ID NO: 238 (see the alignment below). Thus, the DNA of Puttikhunt et al is embraced by the claims (*e.g.*, see claim 1(a)).

Art Unit: 1634

RESULT 32

STMSAM/c

LOCUS STMSAM 2981 bp DNA linear BCT 02-SEP-1997

DEFINITION Streptomyces coelicolor DNA for aspartate
aminotransferase, ribosomal protein, partial and complete cds.

ACCESSION D32254

VERSION D32254.1 GI:971285

KEYWORDS nusG; secE; rplK; rplA; ribosomal protein; aspartate
aminotransferase.

SOURCE Streptomyces coelicolor A3(2)

ORGANISM Streptomyces coelicolor A3(2)

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.

REFERENCE 1 (bases 1 to 2981)

AUTHORS Puttikhunt, C., Nihira, T. and Yamada, Y.

TITLE Cloning, nucleotide sequence, and transcriptional analysis of the
nusG gene of Streptomyces coelicolor A3(2), which encodes a
putative transcriptional antiterminator

JOURNAL Mol. Gen. Genet. 247 (1), 118-122 (1995)

PUBMED 7715599

REFERENCE 2 (bases 1 to 2981)

AUTHORS Puttikhunt, C.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-1994) Chunya Puttikhunt, Osaka University,
Department of Biotechnology; 2-1 Yamadaoka, Suita, Osaka 565, Japan
(Tel: 06-877-5111 (ex. 3441), Fax: 06-879-7448)

COMMENT Submitted (20-Jul-1994) to DDBJ by:

Puttikhunt Chunya

Osaka University

Department of Biotechnology

2-1 Yamadaoka

Suita, Osaka 565

Japan

Phone: 06-877-5111 x3441

Fax: 06-879-7448.

DRDKLYAPLEAVRLAKETSTSKFDGTVEV

AFRLGVDPKADQMVRGTVNLPHTGKTA"

ORIGIN

Alignment Scores:

Pred. No.:	44.2	Length:	2981
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	1	Gaps:	0

US-09-989-890-238 (1-212) x STMSAM (1-2981)

Qy 51 GlyAlaGlyLeuProSerAlaSerAlaAla 60

|||||

Db 1860 GGCGCCGGCTTGCCCTCGGCCTCGGCGGCC 1831

Art Unit: 1634

Claims 1-5, 7-9, 15, and 17 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Williams et al (WO 99/38972 (August 5, 1999)). Williams et al discloses a lung cancer marker DNA of 300 nucleotides length that matches with 300 nucleotides of SEQ ID NO: 105. See the alignment of SEQ ID NO: 105 of the instant application with SEQ ID NO: 861 of Williams et al. Thus, SEQ ID NO: 861 of Williams et al meets claim 1(a)-(d). The DNA of Williams et al would selectively hybridize to SEQ ID NO: 105 of the instant application because maximum duplex stability is reached at 25-50 base pairs (see Kennell (Progr. Nucl. Acid Res. Mol. Biol. 11: 259 (1971)) pages 260-261). Williams et al also teaches the use of vectors and transformed host cells for heterologous expression of nucleic acids (*e.g.*, see pages 15-17 of Williams et al) and the use of nucleic acids *in vivo* (see pages 74-76). It is noted here that claim 8 is construed to not include transgenic organisms because of the necessity of the presence of a vector in the host cell and in view of the definition of "host cell" in the application at page 21, first full paragraph.

RESULT 12

AAZ13392

ID AAZ13392 standard; cDNA; 300 BP.

XX

AC AAZ13392;

XX

DT 12-OCT-1999 (first entry)

XX

DE Human gene expression product cDNA sequence SEQ ID NO:861.

XX

KW Human; gene; gene expression product; diagnosis; therapy; probe;

KW detection; mapping; tissue typing; profiling; forensic; cancer;

KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.

XX

OS Homo sapiens.

XX

PN WO9938972-A2.

XX

PD 05-AUG-1999.

XX

PF 28-JAN-1999; 99WO-US001619.

XX

PR 28-JAN-1998; 98US-0072910P.

PR 24-FEB-1998; 98US-0075954P.

PR 31-MAR-1998; 98US-0080114P.

PR 03-APR-1998; 98US-0080515P.

PR 03-APR-1998; 98US-0080666P.

PR 21-OCT-1998; 98US-0105234P.

PR 28-OCT-1998; 98US-0105877P.

XX

PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
DR WPI; 1999-494092/41.
XX
PT Novel human genes and their expression products which are differentially
PT expressed in different cell types.
XX
PS Claim 1; Page 860; 2479pp; English.
XX
CC The present invention describes a library of human polynucleotides
CC comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one of
CC the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists
XX
SQ Sequence 300 BP; 63 A; 96 C; 90 G; 51 T; 0 U; 0 Other;

Query Match 17.5%; Score 300; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 825 CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGG 884
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGG 60

Qy 885 CCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGAC 944
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGAC 120

Qy 945 CTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGTGCTGCCCTGACAGTGGCCA 1004
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 CTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGTGCTGCCCTGACAGTGGCCA 180

Qy 1005 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGA 1064
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGA 240

Qy 1065 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGC 1124
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGC 300

Art Unit: 1634

Claims 1-3, 7, and 8 are rejected under 35 U.S.C. 102(a) as being clearly anticipated by GenBank® Accession No. AL592304 (July 25, 2001). GenBank® Accession No. AL592304 discloses a DNA that is 60.5% identical to SEQ ID NO: 105 (see the alignment below). Thus, the DNA of GenBank® Accession No. AL592304 is embraced by the claims. Since the DNA of the reference was sequenced, it was necessarily contained within a vector and host cell (claims 7 and 8). GenBank® Accession No. AL592304 is cited as prior art because there is no basis in Serial No. 60/252,509 for SEQ ID NO: 105.

RESULT 9
AL592304
LOCUS AL592304 111738 bp DNA linear HTG 25-JUL-2001
DEFINITION Homo sapiens chromosome 1 clone RP3-426N7, 7 unordered pieces.
ACCESSION AL592304
VERSION AL592304.1 GI:14586390
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Mclay, K.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
COMMENT ----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ426N7
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q30
Consensus quality: 110681 bases at least Q20
Insert size: 111138; sum-of-contigs
Insert size: 119403; 8.4% error; agarose-fp
Quality coverage: 11.23x in Q20 bases; sum-of-contigs Quality
coverage: 10.67x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

Art Unit: 1634

* as soon as it is available and the accession number will
* be preserved.

```
*      1      18058: contig of 18058 bp in length
*      18059   18158: gap of 100 bp
*      18159   35144: contig of 16986 bp in length
*      35145   35244: gap of 100 bp
*      35245   54710: contig of 19466 bp in length
*      54711   54810: gap of 100 bp
*      54811   72936: contig of 18126 bp in length
*      72937   73036: gap of 100 bp
*      73037   92888: contig of 19852 bp in length
*      92889   92988: gap of 100 bp
*      92989   108739: contig of 15751 bp in length
*     108740   108839: gap of 100 bp
*     108840   111738: contig of 2899 bp in length.
```

FEATURES

```

Location/Qualifiers
source      1. .111738
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="1"
            /clone="RP3-426N7"
            /clone_lib="RPCI-3"
misc_feature 1. .18058
            /note="assembly_fragment:02048
            fragment_chain:1
            clone_end:T7
            vector_side:left"
misc_feature 18159. .35144
            /note="assembly_fragment:02454
            fragment_chain:1"
misc_feature 35245. .54710
            /note="assembly_fragment:02786
            fragment_chain:1"
misc_feature 54811. .72936
            /note="assembly_fragment:00223
            fragment_chain:2"
misc_feature 73037. .92888
            /note="assembly_fragment:01820
            fragment_chain:2"
misc_feature 92989. .108739
            /note="assembly_fragment:01122
            fragment_chain:2"
misc_feature 108840. .111738
            /note="assembly_fragment:02919
            fragment_chain:2
            clone_end:SP6
            vector_side:right"

```

ORIGIN

Query Match 60.5%; Score 1035.8; DB 2; Length 111738;
Best Local Similarity 99.8%; Pred. No. 9.7e-250;
Matches 1037; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCGCCCTGGACACCCCGCCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 60
 |||
 Db 95726 ATGCCCGCCCTGGACACCCCGCCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 95785
 Qy 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCACCAAGCCGC 120
 |||

Art Unit: 1634

Db 95786 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCGC 95845

Qy 121 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC 180
|||||

Db 95846 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC 95905

Qy 181 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCACCTGCTGCCTGCTCTGGCGACCC 240
|||||

Db 95906 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCACCTGCTGCCTGCTCTGGCGACCC 95965

Qy 241 TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 300
|||||

Db 95966 TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 96025

Qy 301 CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCTGCCTGTCTACTGAGGACTCCACTGAG 360
|||||

Db 96026 CGCTGTGGAGCCTGTGTGTGGGGATGCAGCCCTGCCTGTCTACTGAGGATTCCACTGAG 96085

Qy 361 GGGACTGCTGAAGCCAAC TGGGCCAAGGAGCACAATGGAGTGCCCCCAGCCCTGATCGT 420
|||||

Db 96086 GGGACTGCTGAAGCCAAC TGGGCCAAGGAGCACAATGGAGTGCCCCCAGCCCTGATCGT 96145

Qy 421 GCACCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC 480
|||||

Db 96146 GCACCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC 96205

Qy 481 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 540
|||||

Db 96206 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 96265

Qy 541 GCCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCACCCATGCGACAC 600
|||||

Db 96266 GCCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCACCCATGCGACAC 96325

Qy 601 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 660
|||||

Db 96326 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 96385

Qy 661 GAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTGAGCCGAGAAATTGAT 720
|||||

Db 96386 GAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTGAGCCGAGAAATTGAT 96445

Qy 721 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTACGCGTACACCAGATCGATGAGCTGGCC 780
|||||

Db 96446 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTACGCGTACACCAGATCGATGAGCTGGCC 96505

Qy 781 AAGTGCACATCAGACACTGTGTTCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 840
|||||

Db 96506 AAGTGCACATCAGACACTGTGTTCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 96565

Qy 841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC 900
|||||

Db 96566 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC 96625

Qy 901 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCGTTCA 960
|||||

Db 96626 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCGTTCA 96685

Qy 961 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGC 1020
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Art Unit: 1634

Db 96686 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC 96745

Qy 1021 TCAGGTCTCAGCCAGGATG 1039

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Db 96746 TCAGGTCTCAGCCAGGATG 96764

Any inquiry concerning this communication or earlier communications from the examiner should be directed to James Martinell whose telephone number is (571) 272-0719.

The examiner works a flexible schedule and can be reached by phone and voice mail. Alternatively, a request for a return telephone call may be e-mailed to james.martinell@uspto.gov. Since e-mail communications may not be secure, it is suggested that information in such requests be limited to name, phone number, and the best time to return the call.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla, can be reached on (571) 272-0735.

OFFICIAL FAX NUMBER


The fax phone number for the organization where this application or proceeding is assigned is (571) 273-8300. Any Official Communication to the USPTO should be faxed to this number.

Art Unit: 1634

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James Martinell, Ph.D.
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